With this amendment, claims 19-22 are amended, claims 34 and 35 are cancelled without prejudice or disclaimer, and new claims 38 and 39 have been added. Claims 1-4, 7-33, and 36-39 are pending in the application.

Claims 19-22 have been amended to delete the expression "capable of".

New claims 38 and 39 are directed to methods of selecting a soybean plant having a deletion in a peroxidase gene based on a comparison to an EpEp genotype. These new claims are supported by claim 35. Further support for these new claims may be found, for example, in Examples 2 and 3, and Figures 4-8. Figure 4 demonstrates restriction length fragment polymorphisms between the two plant genotypes, Figure 5 shows a deletion in a peroxidase sequence between the two genotypes corresponding to nucleotides 1524 and 1610 of SEQ ID NO:2, and Figures 6-8 which demonstrate PCR analysis of the two genotypes. Applicant submits that no new matter has been introduced into the application as a result of these amendments.

Rejection under 35 U.S.C. §112 and 35 U.S.C. §101

Claims 34 and 35 have been rejected to under 35 USC 112 and 35 USC 101 as lacking method/process steps and therefore being indefinite and improperly defining a process.

Applicant has cancelled claims 34 and 35 without prejudice or disclaimer, and therefore requests withdrawal of Examiner's rejection.

Rejection under 35 U.S.C. §103

Claims 19-22 have been rejected under 35 USC 103 as unpatentable over Knauf et al.

Examiner states "that this rejection is based on a lack of requirement of DNA expression" Applicant has amended claims 19-22 to delete the expression "capable of". Applicant submits that claims 19-22, as presently amended, recite a requirement of DNA expression. Accordingly, Applicant requests that rejection of claims 19-22 under 35 USC 103 be withdrawn.

ALLOWABLE SUBJECT MATTER

Examiner has indicated that claims 1-4, 7-18, 23-33, 36 and 37are allowable.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned **"Version with markings to show changes made"**.

This application is submitted to be in condition for allowance and a Notice to that effect is requested. Should the Examiner believe that anything further is desirable in order to place the application in better condition for allowance, the Examiner is invited to contact the undersigned at the telephone number listed below.

Respectfully submitted

By Mary J. Wilson

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

The paragraph beginning at page 9, line 4:

[**Figure 1** is] **Figures 1A and 1B** are the cDNA and deduced amino acid sequence of soybean seed coat peroxidase. Nucleotides are numbered by assigning +1 to the first base of the ATG start codon; amino acids are numbered by assigning +1 to the N-terminal Gln residue after cleavage of the putatuve signal sequence. The N-terminal signal sequence, the region of the active site, and the heme-binding domain are underlined. The numerals I, II and III placed directly above signal nucleotide gaps in the sequence indicate the three intron splice positions. The target site and direction of five different PCR primers are shown with dotted lines above the nucleotide sequence. An asterisk (*) marks the translation stop codon.

The paragraph beginning at page 9, line 14:

[**Figure 2** is] **Figures 2A and 2B** are the genomic DNA sequence of the Soybean seed coat peroxidase.

The paragraph beginning at page 9, line 16:

[**Figure 3** is] **Figures 3A-(1)-3A(4) and 3B** are a comparison of soybean seed coat peroxidase with other closely related plant peroxidases. The GenBank accession numbers are provided next to the name of the plant from which the peroxidase was isolated. The accession number for the soybean sequence is L78163. [(A)] (Fig. 3A-(1)-3A-(4)) A comparison of the nucleic acid sequences; [(B)] (Fig. 3B) A comparison of the amino acid sequences.

The paragraph beginning at page 11, line 3:

[**Figure 7** exhibits] **Figures 7A and 7B** exhibit PCR analysis of an F2 population from a cross of *EpEp* and *epep* genotypes. Genomic DNA was used as template for PCR analysis of the parents (P) and 30 F_2 individuals. The cross was derived from the soybean lines OX312 (*epep*) and OX347 (*EpEp*). Plants were self pollinated and seeds were collected and scored for seed coat peroxidase activity. The symbols (-) and (+) indicate low and high seed coat peroxidase activity, respectively. Primers prx9+ and prx10- were used in the amplification reactions. Products were separated by electrophoresis through a 0.8% agarose gel and visualized under UV light after staining with ethidium bromide. The migration of molecular markers and their corresponding size in kb is also shown (lanes M).

The paragraph beginning at page 11, line 14:

[**Figure 8** displays] **Figures 8A-8C** display PCR analysis of six different soybean cultivars with primers derived from the seed coat peroxidase cDNA sequence. Genomic

DNA was used as template for PCR analysis of three *EpEp* cultivars and three *epep* cultivars. Primers used in the amplification reactions and the size of the DNA product is indicated on the left. Products were separated by electrophoresis through a 0.8% agarose gel and visualized under UV light after staining with ethidium bromide.

[**(A)**] **(Fig. 8A)** Forward and reverse primers are downstream from deletion

[**(B)**] **(Fig. 8B)** Forward primer anneals to site within deletion

[**(C)**] **(Fig. 8C)** Primers span deletion

The paragraph beginning at page 12, line 2:

[**Figure 9** shows] **Figures 9A and 9B** show the accumulation of peroxidase RNA in tissues of GEp and *epep* plants. **Figure 9(A)**: A comparison of peroxidase transcript abundance in cultivars Harosoy 63 (Ep) or Marathon (ep). Seed and pod tissues were sampled at a late stage of development corresponding to a whole seed fresh weight of 250 mg. Root and leaf tissue was from six week old plants. Autoradiograph exposed for 96 h. **Figure 9(B)**: Developmental expression of peroxidase in cultivar Harosoy 63 (EP). Flowers were sampled immediately after opening. Seed coat tissues were sampled at four stages of development corresponding to a whole seed fresh weight of: lane 1, 50 mg; lane 2, 100 mg; lane 3, 200 mg; lane 4, 250 mg. Autoradiograph exposed for 20 h.

IN THE CLAIMS:

Claims 19-22 have been amended as follows:

19. (Amended) A host cell [~~capable of~~] expressing the DNA molecule within the vector of claim 15.

20. (Twice Amended) A transgenic seed coat cell [~~capable of~~] expressing a gene of interest under control of a regulatory region, wherein the gene of interest and regulatory region are contained within the vector of claim 16.

21. (Amended) A host cell [~~capable of~~] expressing the DNA molecule within the vector of claim 17.

(Twice Amended) A transgenic seed coat cell [~~capable of~~] expressing the DNA molecule within the vector of claim 18.